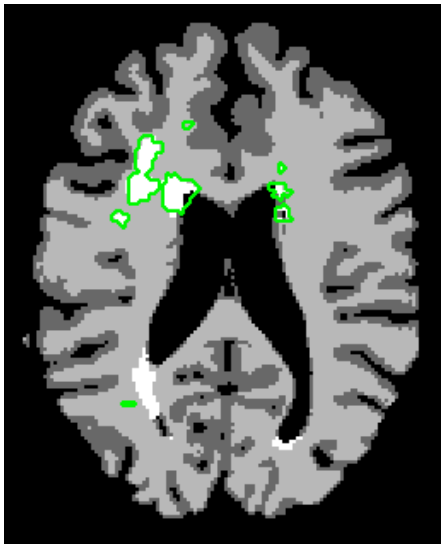
Detecting White Matter Lesions in Lupus



Version 2.0
1/6/2009

H. Jeremy Bockholt
Mark Scully

Learning objective

Following this tutorial, you'll be able to load scans into Slicer3, and segment and measure the volume of white matter lesions on the provided data-set.

Prerequisites

This tutorial assumes that you have already completed the tutorial **Data Loading and Visualization**. Tutorials for **Slicer3** are available at the following location:

- **Slicer3** tutorials
http://www.na-mic.org/Wiki/index.php/Slicer3.2:Training

Material

This course requires the following installation:

- The current version of Slicer 3.3.x Software (*built from source*), which can be installed from:
  - http://www.slicer.org/pages/Downloads
- The White Matter Lesion module extension to Slicer 3, which can be download from:
  - http://www.nitrc.org/frs/download.php/570/LesionSegmentationApplications.tgz
- The Lupus Lesion Tutorial Data, which can be downloaded from:
  - http://www.nitrc.org/frs/download.php/569/LesionSegmentationTutorialData.tgz
- n.b., a reliable internet connection will be required for downloading the data

Disclaimer

It is the responsibility of the user of 3DSlicer to comply with both the terms of the license and with the applicable laws, regulations and rules.

Methods

Approximately 90 features were computed based on the T1, T2, and FLAIR, including neighborhood means with varying radii, mathematical morphometry dilation and erosion, kmeans clustering, and gradients, among others. **Adaboost** was applied to the data to find the 20 features that best discriminate lesion from non-lesion. Those 20 features were then calculated for all lesions, for all subjects, then zero-meaned and the standard deviation was set to one. The centroid of the lesions was then calculated and the max distance found between the centroid and the lesion voxels. The max distance threshold was used to exclude voxels that had no chance of being lesions. The features for all voxels within the distance threshold were calculated and scaled to a range of negative one to positive one. The means and covariance of these features were calculated for both the lesion and non-lesion classes and used to define the two classes in a **Bayesian classifier**. A parameter search was then performed to find the prior that gave the best combination of Specificity and Sensitivity.

When classifying, the 20 relevant features are calculated, zero-meaned and sigma set to one, thresholded based on the distance to the lesion centroid, and then passed to the Bayesian classifier.

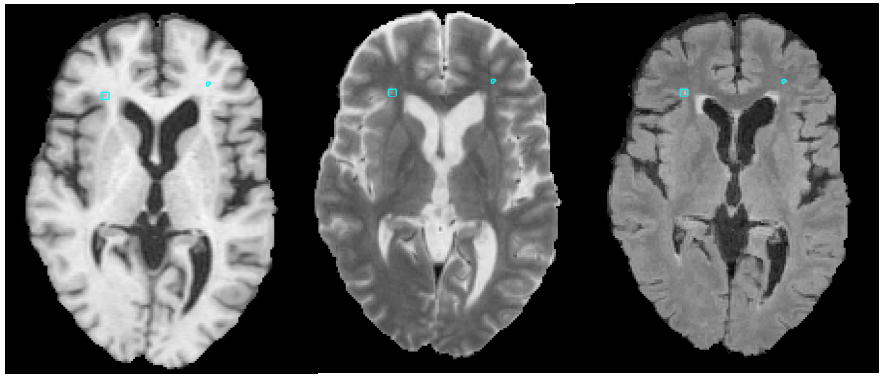
Module Setup

- If Slicer has been built from source on your platform, the lupus lesion module needs to be unzipped in the **Slicer3/Applications/CLI/ directory** and
  - "**subdirs (LesionSegmentationApplications)**"
    - needs to be added to the **Slicer3/Applications/CLI/CMakeLists.txt**
    - If you search in that file for other "subdirs(*)" statements you can just put it above one of the others.
  - Then you need to go to Slicer3-build/ and type "make".

Data

This course is built upon two scans of patients with lupus that have T1, T2, and FLAIR images. These images have been co-registered and brain extracted.

The following summary shows the contents of the data/LesionSegmentationTutorial directory once download and uncompressed

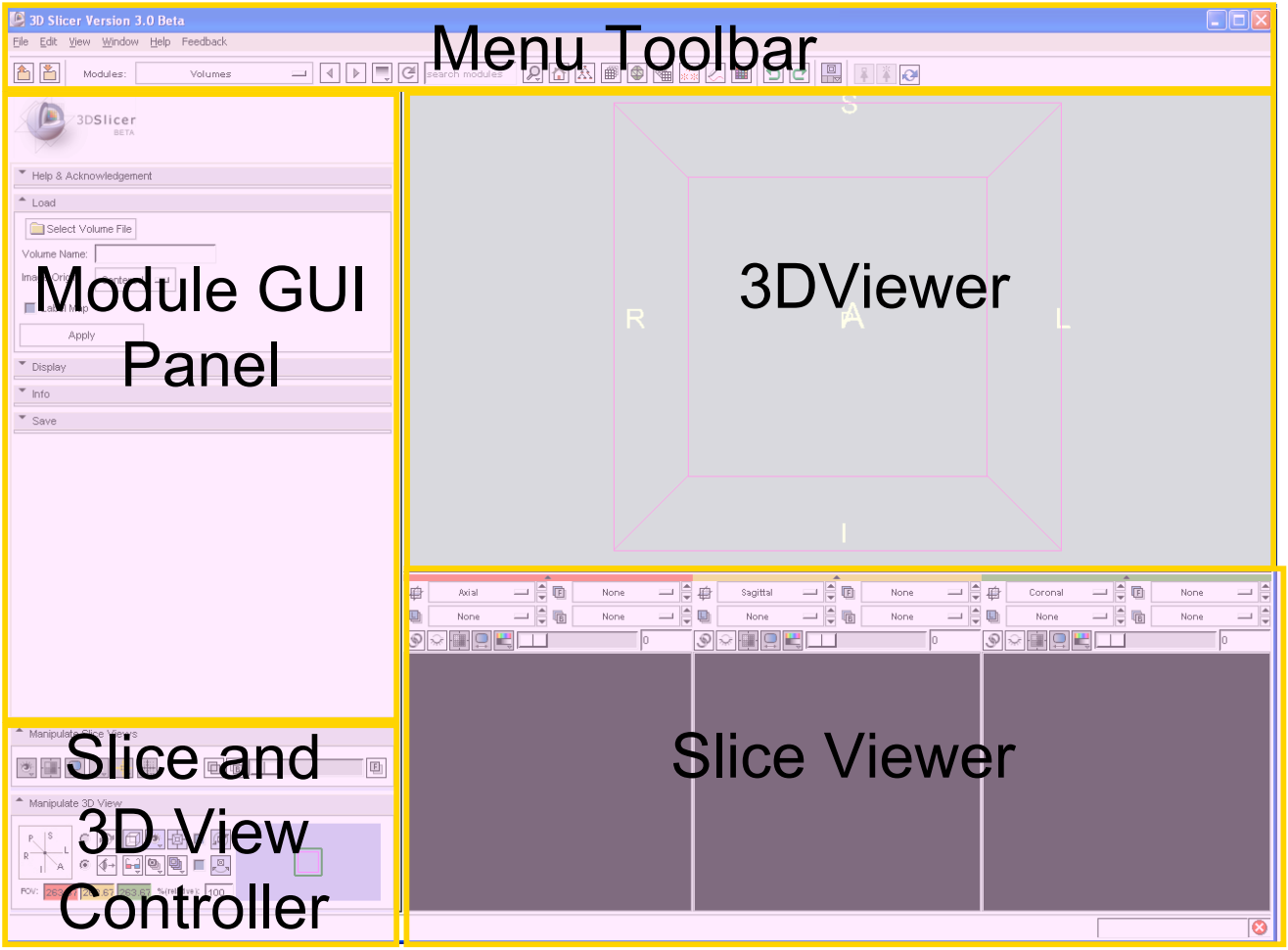


lupus002_FLAIR_reg+bias.nii.gz
lupus002_T1_reg+bias.nii.gz
lupus002_T2_reg+bias.nii.gz
lupus002_brain_mask.nii.gz
lupus003_FLAIR_reg+bias.nii.gz
lupus003_T1_reg+bias.nii.gz
lupus003_T2_reg+bias.nii.gz
lupus003_brain_mask.nii.gz

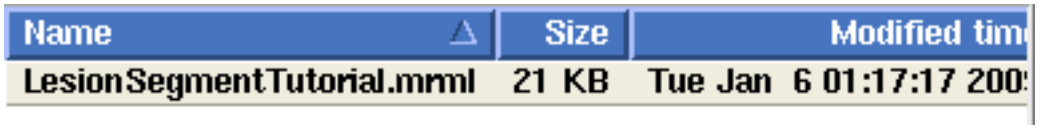
Slicer3 GUI

The Graphical User Interface (GUI) of Slicer3 integrates five components:

- the Menu Toolbar
- the Module GUI Panel
- the 3D Viewer
- the Slice Viewer
- the Slice and 3D View Controller



Step 1: Loading the Data

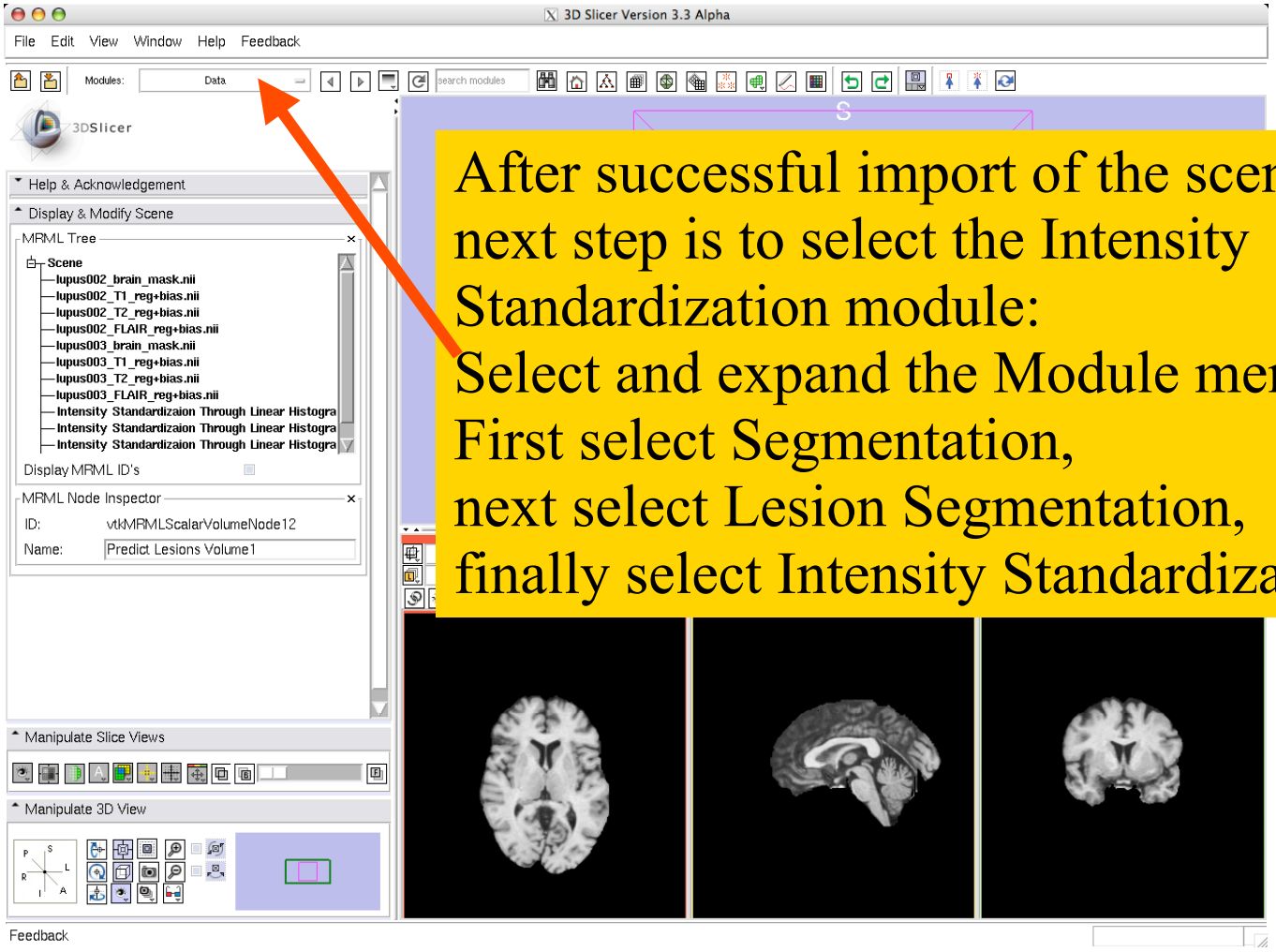


Import the scene by selecting File Import Scene feature from the menu.

Navigate the filesystem to locate the MRML scene that you have downloaded.

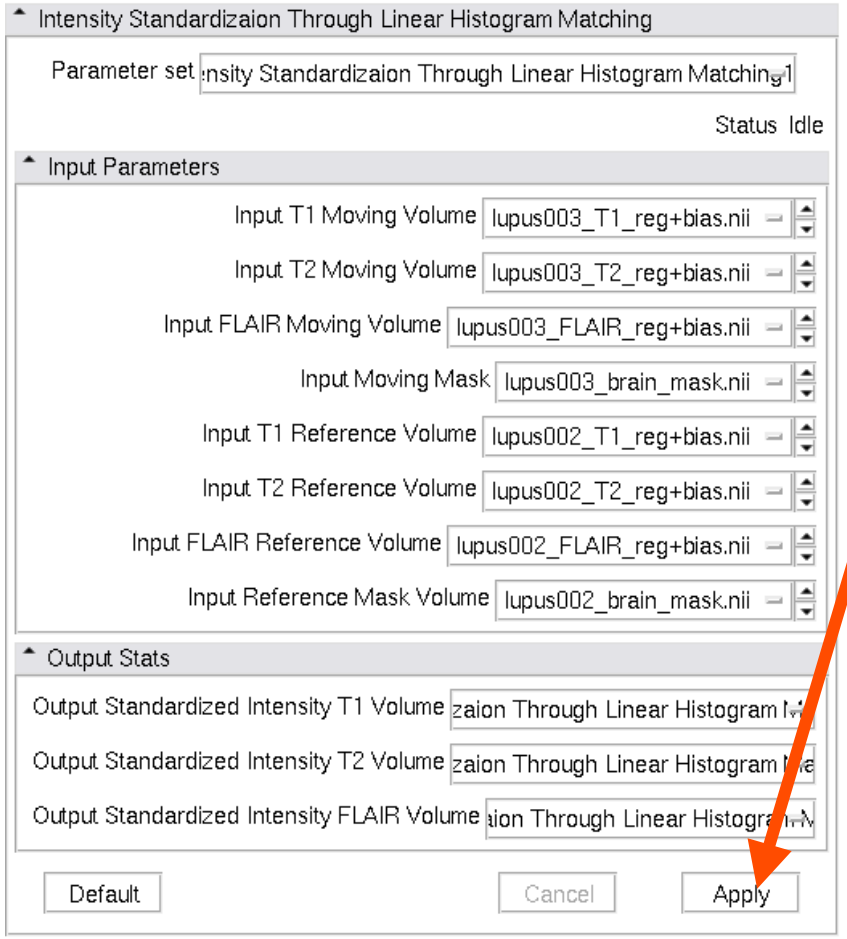
By loading the scene you will load the reference data sets that are needed for this tutorial.

Step 2



After successful import of the scene, the next step is to select the Intensity Standardization module:
Select and expand the Module menu,
First select Segmentation,
next select Lesion Segmentation,
finally select Intensity Standardization.

Step 3

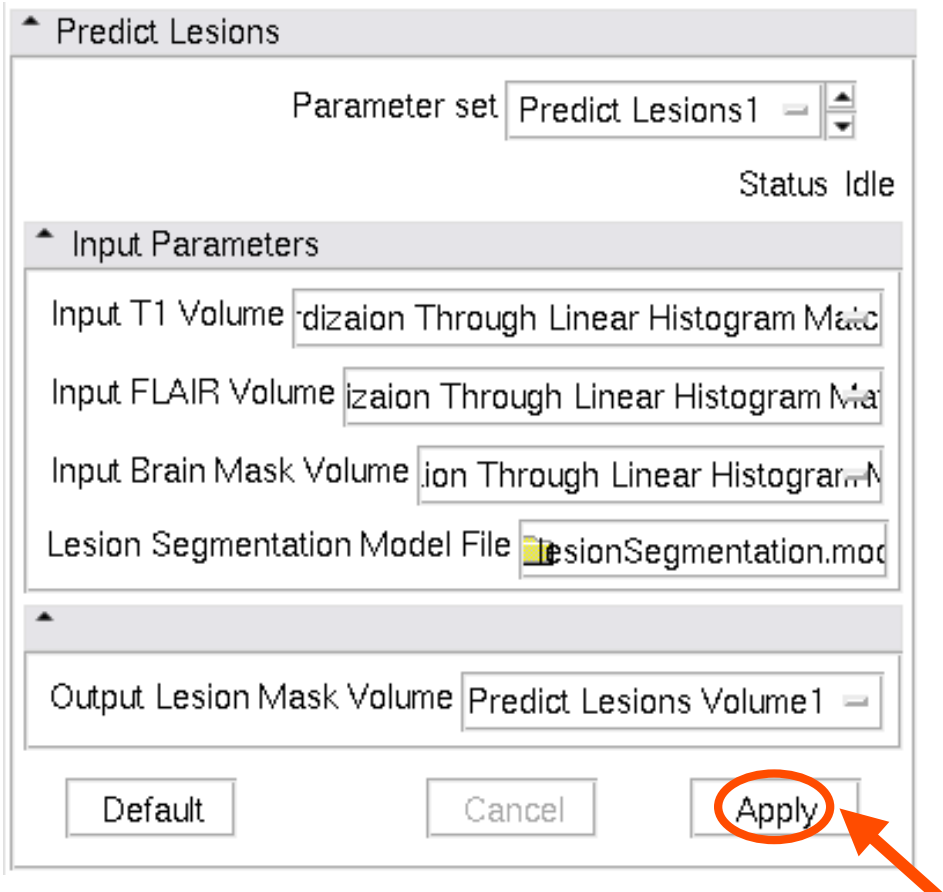


By nature of importing the MRML scence, the input parameters to the Intensity Standardization Module should be automatically populated. Thus, once loaded simply

Click "Apply"

This step should take approximately 2 minutes; however, progress can be monitored through the progress monitor on the bottom left of the main Slicer GUI.

Step 4



The next step is to select and execute the Predict Lesion module. You will find this module beneath the Segmentation, Lesion Segmentation in the hierarchical Module menu.

The imported MRML scene will automatically populate the input parameters. You may need to select the LesionSegmentation.model file manually from the same directory that you loaded the MRML scene from. Once all parameters are populated, run the module by

Clicking "Apply"

Conclusion

- Since the tool has produced a label map, you may now measure the volumes of the automatically labeled lesion tissue.
- This capability provides an intuitive graphical user interface to interact with the data
- The tool has been built in an open-source environment and is readily available to the scientific community

For More Information

- Register as a user of this 3dSlicer Module using the NITRC resource to keep updated on any changes or additions to either the capability or tutorial
  - http://www.nitrc.org/projects/lupuslesion/
- You may also send e-mail message with any questions or concerns to Jeremy Bockholt (jbockholt@mrn.org)

Acknowledgments

National Alliance for Medical Image Computing
NIH U54EB005149

And other support:

DOE DE-FG02-99ER6274
NIH 5R01HL077422-02
NIH P41 RR13218
NIH U24-RR021992